

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Rice MLH1 Ortholog and Uses Thereof

<130> 35718/238971

<150> 60/233,124

<151> 2000-09-18

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2501

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (121)...(2295)

<400> 1

```

cggcacgaga ttttgcagtc tcctctcctc ctccgctcga gcgagtgagt cccgaccacg      60
tcgctgccct cgctcaccg ccggccaacc gccgtgacga gagatcgagc agggcggggc      120
atg gac gag cct tcg ccg cgc gga ggt ggg tgc gcc ggg gag ccg ccc      168
Met Asp Glu Pro Ser Pro Arg Gly Gly Cys Ala Gly Glu Pro Pro
   1           5           10          15

cgc atc cgg agg ttg gag gag tcg gtg gtg aac cgc atc gcg gcg ggg      216
Arg Ile Arg Arg Leu Glu Glu Ser Val Val Asn Arg Ile Ala Ala Gly
           20           25           30

gag gtg atc cag cgg ccg tcg tcg gcg gtg aag gag ctc atc gag aac      264
Glu Val Ile Gln Arg Pro Ser Ser Ala Val Lys Glu Leu Ile Glu Asn
           35           40           45

agc ctc gac gct ggc gcc tcc agc gtc tcc gtt gcg gtg aag gac ggt      312
Ser Leu Asp Ala Gly Ala Ser Ser Val Ser Val Ala Val Lys Asp Gly
           50           55           60

ggc ctc aag ctc atc cag gtc tcc gat gac ggc cat ggc atc agg ttt      360
Gly Leu Lys Leu Ile Gln Val Ser Asp Asp Gly His Gly Ile Arg Phe
           65           70           75           80

gag gat ttg gca ata ttg tgc gaa agg cat act acc tca aag tta tct      408
Glu Asp Leu Ala Ile Leu Cys Glu Arg His Thr Thr Ser Lys Leu Ser
           85           90           95

gca tac gag gat ctg cag acc ata aaa tcg atg ggg ttc aga ggg gag      456
Ala Tyr Glu Asp Leu Gln Thr Ile Lys Ser Met Gly Phe Arg Gly Glu
           100           105           110

```

gct ttg gct agt atg act tat gtt ggc cat gtt acc gtg aca acg ata	504
Ala Leu Ala Ser Met Thr Tyr Val Gly His Val Thr Val Thr Thr Ile	
115 120 125	
aca gaa ggc caa ttg cac ggc tac agg gtt tct tac aga gat ggt gta	552
Thr Glu Gly Gln Leu His Gly Tyr Arg Val Ser Tyr Arg Asp Gly Val	
130 135 140	
atg gag aat gag cct aag cct tgc gct gcg gtg aaa gga act caa gtc	600
Met Glu Asn Glu Pro Lys Pro Cys Ala Ala Val Lys Gly Thr Gln Val	
145 150 155 160	
atg gtt gaa aat cta ttt tac aac atg gta gcc cgc aag aaa aca ttg	648
Met Val Glu Asn Leu Phe Tyr Asn Met Val Ala Arg Lys Lys Thr Leu	
165 170 175	
cag aac tcc aat gat gac tac ccc aag atc gta gac ttc atc agt cgg	696
Gln Asn Ser Asn Asp Asp Tyr Pro Lys Ile Val Asp Phe Ile Ser Arg	
180 185 190	
ttt gca gtc cat cac atc aac gtt acc ttc tct tgc aga aag cat gga	744
Phe Ala Val His His Ile Asn Val Thr Phe Ser Cys Arg Lys His Gly	
195 200 205	
gcc aat aga gca gat gtt cat agt gca agt aca tcc tca agg tta gat	792
Ala Asn Arg Ala Asp Val His Ser Ala Ser Thr Ser Ser Arg Leu Asp	
210 215 220	
gct atc agg agt gtc tat ggg gct tct gtc gtt cgt gat ctc ata gaa	840
Ala Ile Arg Ser Val Tyr Gly Ala Ser Val Val Arg Asp Leu Ile Glu	
225 230 235 240	
ata aag gtt tca tat gag gat gct gca gat tca atc ttc aag atg gat	888
Ile Lys Val Ser Tyr Glu Asp Ala Ala Asp Ser Ile Phe Lys Met Asp	
245 250 255	
ggg tac atc tca aat gca aat tat gtg gca aag aag att aca atg att	936
Gly Tyr Ile Ser Asn Ala Asn Tyr Val Ala Lys Lys Ile Thr Met Ile	
260 265 270	
ctt ttc ata aat gat agg ctt gta gac tgt act gct ttg aaa aga gct	984
Leu Phe Ile Asn Asp Arg Leu Val Asp Cys Thr Ala Leu Lys Arg Ala	
275 280 285	
att gaa ttt gtg tac tct gca aca ttg cct caa gca tcc aaa cct ttc	1032
Ile Glu Phe Val Tyr Ser Ala Thr Leu Pro Gln Ala Ser Lys Pro Phe	
290 295 300	
ata tac atg tcc ata cat ctt cca tca gaa cac gtg gat gtt aat ata	1080
Ile Tyr Met Ser Ile His Leu Pro Ser Glu His Val Asp Val Asn Ile	
305 310 315 320	
cac cca acc aag aaa gag gtt agc ctt ttg aat caa gag cgt att att	1128
His Pro Thr Lys Lys Glu Val Ser Leu Leu Asn Gln Glu Arg Ile Ile	
325 330 335	

gaa aca ata aga aat gct att gag gaa aaa ctg atg aat tct aat aca	1176
Glu Thr Ile Arg Asn Ala Ile Glu Glu Lys Leu Met Asn Ser Asn Thr	
340 345 350	
acc agg ata ttc caa act cag gca tta aac tta tca ggg att gct caa	1224
Thr Arg Ile Phe Gln Thr Gln Ala Leu Asn Leu Ser Gly Ile Ala Gln	
355 360 365	
gct aac cca caa aag gat aag gtt tct gag gcc agt atg ggt tct gga	1272
Ala Asn Pro Gln Lys Asp Lys Val Ser Glu Ala Ser Met Gly Ser Gly	
370 375 380	
aca aaa tct caa aaa att cct gtg agc caa atg gtc aga aca gat cca	1320
Thr Lys Ser Gln Lys Ile Pro Val Ser Gln Met Val Arg Thr Asp Pro	
385 390 395 400	
cgc aat cca tct gga aga ttg cac acc tac tgg cac ggg caa tct tca	1368
Arg Asn Pro Ser Gly Arg Leu His Thr Tyr Trp His Gly Gln Ser Ser	
405 410 415	
aat ctt gaa aag aaa ttt gat ctt gta tct gta aga aat gtt gta aga	1416
Asn Leu Glu Lys Lys Phe Asp Leu Val Ser Val Arg Asn Val Val Arg	
420 425 430	
tca agg aga aac caa aaa gat gct ggt gat ttg tca agc cgt cat gag	1464
Ser Arg Arg Asn Gln Lys Asp Ala Gly Asp Leu Ser Ser Arg His Glu	
435 440 445	
ctc ctt gtg gaa ata gat tct agc ttc cat cct ggc ctt ttg gac att	1512
Leu Leu Val Glu Ile Asp Ser Ser Phe His Pro Gly Leu Leu Asp Ile	
450 455 460	
gtc aag aac tgc aca tat gtt gga ctt gcc gat gaa gcc ttt gct ttg	1560
Val Lys Asn Cys Thr Tyr Val Gly Leu Ala Asp Glu Ala Phe Ala Leu	
465 470 475 480	
ata caa cac aat acc cgc tta tac ctt gta aat gtg gta aat att agt	1608
Ile Gln His Asn Thr Arg Leu Tyr Leu Val Asn Val Val Asn Ile Ser	
485 490 495	
aaa gaa ctt atg tac cag caa gct ttg tgc cgt ttt ggg aac ttc aat	1656
Lys Glu Leu Met Tyr Gln Gln Ala Leu Cys Arg Phe Gly Asn Phe Asn	
500 505 510	
gct att cag ctc agt gaa cca gct cca ctt cag gag ttg ctg gtg atg	1704
Ala Ile Gln Leu Ser Glu Pro Ala Pro Leu Gln Glu Leu Leu Val Met	
515 520 525	
gca ctg aaa gac gat gaa ttg atg agt gat gaa aag gat gat gag aaa	1752
Ala Leu Lys Asp Asp Glu Leu Met Ser Asp Glu Lys Asp Asp Glu Lys	
530 535 540	
ctg gag att gca gaa gta aac act gag ata cta aaa gaa aat gct gag	1800
Leu Glu Ile Ala Glu Val Asn Thr Glu Ile Leu Lys Glu Asn Ala Glu	
545 550 555 560	

atg att aat gag tac ttt tct att cac att gat caa gat ggc aaa ttg 1848
Met Ile Asn Glu Tyr Phe Ser Ile His Ile Asp Gln Asp Gly Lys Leu
565 570 575

aca aga ctt cct gtt gta ctg gac cag tac acc cct gat atg gac cgt 1896
Thr Arg Leu Pro Val Val Leu Asp Gln Tyr Thr Pro Asp Met Asp Arg
580 585 590

ctt cca gaa ttt gtg ttg gct tta gga aat gat gtt act tgg gat gac 1944
Leu Pro Glu Phe Val Leu Ala Leu Gly Asn Asp Val Thr Trp Asp Asp
595 600 605

gag aaa gag tgc ttc aga aca gta gct tct gct gta gga aac ttc tat 1992
Glu Lys Glu Cys Phe Arg Thr Val Ala Ser Ala Val Gly Asn Phe Tyr
610 615 620

gca ctt cat ccc cca atc ctt cca aat cca tct ggg aat ggc att cat 2040
Ala Leu His Pro Pro Ile Leu Pro Asn Pro Ser Gly Asn Gly Ile His
625 630 635 640

tta tac aag aaa aat aga gat tca atg gct gat gaa cat gct gag aat 2088
Leu Tyr Lys Lys Asn Arg Asp Ser Met Ala Asp Glu His Ala Glu Asn
645 650 655

gat cta ata tca gat gaa aat gac gtt gat caa gaa ctt ctt gcg gaa 2136
Asp Leu Ile Ser Asp Glu Asn Asp Val Asp Gln Glu Leu Leu Ala Glu
660 665 670

gca gaa gca gca tgg gcc caa cgt gag tgg acc att cag cat gtc ttg 2184
Ala Glu Ala Ala Trp Ala Gln Arg Glu Trp Thr Ile Gln His Val Leu
675 680 685

ttt cca tcc atg cga ctt ttc ctc aag ccc ccg aag tca atg gca aca 2232
Phe Pro Ser Met Arg Leu Phe Leu Lys Pro Pro Lys Ser Met Ala Thr
690 695 700

gat gga acg ttt gtg cag gtt gct tcc ttg gag aaa ctc tac aag att 2280
Asp Gly Thr Phe Val Gln Val Ala Ser Leu Glu Lys Leu Tyr Lys Ile
705 710 715 720

ttt gaa agg tgt tag ctcataagtg agaaaatgaa ggcagagtaa gatcatgatt 2335
Phe Glu Arg Cys *

catggagtgt ttttgaaaaat gtgtataaatt tcaccgtatt atgtactttg atagtgtctg 2395
tagaaactga agaaagaaaag atggcttttac ttctgaattg aaagttaacg atgccagcaa 2455
ttgtatatattc tgatcaacca aaaaaaaaaa aaaaaaaaaa aaaaaaa 2501

<210> 2

<211> 724

<212> PRT

<213> Oryza sativa

<400> 2

Met Asp Glu Pro Ser Pro Arg Gly Gly Gly Cys Ala Gly Glu Pro Pro
1 5 10 15
Arg Ile Arg Arg Leu Glu Glu Ser Val Val Asn Arg Ile Ala Ala Gly

Ile Gln His Asn Thr Arg Leu Tyr Leu Val Asn Val Val Asn Ile Ser
 485 490 495
 Lys Glu Leu Met Tyr Gln Gln Ala Leu Cys Arg Phe Gly Asn Phe Asn
 500 505 510
 Ala Ile Gln Leu Ser Glu Pro Ala Pro Leu Gln Glu Leu Leu Val Met
 515 520 525
 Ala Leu Lys Asp Asp Glu Leu Met Ser Asp Glu Lys Asp Asp Glu Lys
 530 535 540
 Leu Glu Ile Ala Glu Val Asn Thr Glu Ile Leu Lys Glu Asn Ala Glu
 545 550 555 560
 Met Ile Asn Glu Tyr Phe Ser Ile His Ile Asp Gln Asp Gly Lys Leu
 565 570 575
 Thr Arg Leu Pro Val Val Leu Asp Gln Tyr Thr Pro Asp Met Asp Arg
 580 585 590
 Leu Pro Glu Phe Val Leu Ala Leu Gly Asn Asp Val Thr Trp Asp Asp
 595 600 605
 Glu Lys Glu Cys Phe Arg Thr Val Ala Ser Ala Val Gly Asn Phe Tyr
 610 615 620
 Ala Leu His Pro Pro Ile Leu Pro Asn Pro Ser Gly Asn Gly Ile His
 625 630 635 640
 Leu Tyr Lys Lys Asn Arg Asp Ser Met Ala Asp Glu His Ala Glu Asn
 645 650 655
 Asp Leu Ile Ser Asp Glu Asn Asp Val Asp Gln Glu Leu Leu Ala Glu
 660 665 670
 Ala Glu Ala Ala Trp Ala Gln Arg Glu Trp Thr Ile Gln His Val Leu
 675 680 685
 Phe Pro Ser Met Arg Leu Phe Leu Lys Pro Pro Lys Ser Met Ala Thr
 690 695 700
 Asp Gly Thr Phe Val Gln Val Ala Ser Leu Glu Lys Leu Tyr Lys Ile
 705 710 715 720
 Phe Glu Arg Cys

<210> 3
 <211> 2381
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (3)...(2213)

<400> 3
 ag atg atc gac gat tcg tct ctt acg gcg gag atg gag gag gaa gaa 47
 Met Ile Asp Asp Ser Ser Leu Thr Ala Glu Met Glu Glu Glu Glu
 1 5 10 15
 tct ccg gcg acg acg att gta ccg aga gag cca ccg aag att caa cgc 95
 Ser Pro Ala Thr Thr Ile Val Pro Arg Glu Pro Pro Lys Ile Gln Arg
 20 25 30
 tta gaa gaa tca gta gtc aac cgt atc gca gct ggt gaa gta atc cag 143
 Leu Glu Glu Ser Val Val Asn Arg Ile Ala Ala Gly Glu Val Ile Gln
 35 40 45

cgt cca gtt tca gct gtg aaa gag ctc gtt gag aac agc ctc gac gcc	191
Arg Pro Val Ser Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala	
50 55 60	
gat tca agt tcc ata agc gtc gtt gtc aaa gac ggt ggt ttg aaa ctc	239
Asp Ser Ser Ser Ile Ser Val Val Val Lys Asp Gly Gly Leu Lys Leu	
65 70 75	
att caa gtc tcc gac gac ggt cac ggt att aga cgt gaa gac ttg ccg	287
Ile Gln Val Ser Asp Asp Gly His Gly Ile Arg Arg Glu Asp Leu Pro	
80 85 90 95	
ata cta tgc gag aga cat aca aca tcg aag ctg act aag ttt gag gat	335
Ile Leu Cys Glu Arg His Thr Thr Ser Lys Leu Thr Lys Phe Glu Asp	
100 105 110	
ttg ttc tct ctg agt tca atg gga ttt aga gga gag gca tta gct agt	383
Leu Phe Ser Leu Ser Ser Met Gly Phe Arg Gly Glu Ala Leu Ala Ser	
115 120 125	
atg acc tat gtt gct cat gtt aca gtg act act att act aaa ggc cag	431
Met Thr Tyr Val Ala His Val Thr Val Thr Thr Ile Thr Lys Gly Gln	
130 135 140	
att cat ggt tat aga gtg tct tat aga gat ggt gtc atg gag cat gaa	479
Ile His Gly Tyr Arg Val Ser Tyr Arg Asp Gly Val Met Glu His Glu	
145 150 155	
cca aag gcg tgt gct gct gtc aaa gga aca cag ata atg gtg gag aat	527
Pro Lys Ala Cys Ala Ala Val Lys Gly Thr Gln Ile Met Val Glu Asn	
160 165 170 175	
ttg ttc tac aat atg att gct aga agg aag aca ctt caa aat tct gct	575
Leu Phe Tyr Asn Met Ile Ala Arg Arg Lys Thr Leu Gln Asn Ser Ala	
180 185 190	
gat gat tac ggg aaa atc gtg gat ttg ctg agc cgg atg gct att cat	623
Asp Asp Tyr Gly Lys Ile Val Asp Leu Leu Ser Arg Met Ala Ile His	
195 200 205	
tac aat aat gtc agc ttt tct tgt cga aag cat gga gct gtt aag gct	671
Tyr Asn Asn Val Ser Phe Ser Cys Arg Lys His Gly Ala Val Lys Ala	
210 215 220	
gat gtt cac tca gtc gtg tca cct tca agg ctt gat tca att agg tct	719
Asp Val His Ser Val Val Ser Pro Ser Arg Leu Asp Ser Ile Arg Ser	
225 230 235	
gta tat gga gta tca gtt gca aag aac ttg atg aaa gta gaa gtt tcc	767
Val Tyr Gly Val Ser Val Ala Lys Asn Leu Met Lys Val Glu Val Ser	
240 245 250 255	
tcc tgt gac tcc tct ggt tgt act ttt gat atg gag ggt ttc ata tcc	815
Ser Cys Asp Ser Ser Gly Cys Thr Phe Asp Met Glu Gly Phe Ile Ser	
260 265 270	

aat tct aac tat gtt gct aag aag act ata ttg gtg ctt ttc att aat	863
Asn Ser Asn Tyr Val Ala Lys Lys Thr Ile Leu Val Leu Phe Ile Asn	
275 280 285	
gat aga ttg gtg gaa tgc tct gcc tta aaa aga gcc att gaa att gtt	911
Asp Arg Leu Val Glu Cys Ser Ala Leu Lys Arg Ala Ile Glu Ile Val	
290 295 300	
tat gct gca aca ttg cca aaa gca tca aaa cct ttt gtc tac atg tca	959
Tyr Ala Ala Thr Leu Pro Lys Ala Ser Lys Pro Phe Val Tyr Met Ser	
305 310 315	
atc aat ttg cca cgg gaa cat gtt gat atc aat att cac cca aca aag	1007
Ile Asn Leu Pro Arg Glu His Val Asp Ile Asn Ile His Pro Thr Lys	
320 325 330 335	
aaa gag gtt agc ctt cta aac cag gaa atc att att gag atg ata cag	1055
Lys Glu Val Ser Leu Leu Asn Gln Glu Ile Ile Ile Glu Met Ile Gln	
340 345 350	
tca gag gtt gaa gta aaa ctg aga aac gca aat gat act agg acg ttt	1103
Ser Glu Val Glu Val Lys Leu Arg Asn Ala Asn Asp Thr Arg Thr Phe	
355 360 365	
caa gag cag aaa gtg gaa tac att caa tct acg tta aca tct cag aaa	1151
Gln Glu Gln Lys Val Glu Tyr Ile Gln Ser Thr Leu Thr Ser Gln Lys	
370 375 380	
agt gat tct cca gtt tct cag aag cct tct gga caa aag aca cag aaa	1199
Ser Asp Ser Ser Pro Val Ser Gln Lys Pro Ser Gly Gln Lys Thr Gln Lys	
385 390 395	
gtt cct gtg aac aaa atg gtg aga aca gat tca tca gat cca gct gga	1247
Val Pro Val Asn Lys Met Val Arg Thr Asp Ser Ser Asp Pro Ala Gly	
400 405 410 415	
agg tta cat gcc ttt ttg caa ccc aag cca caa agt ctc cct gac aag	1295
Arg Leu His Ala Phe Leu Gln Pro Lys Pro Gln Ser Leu Pro Asp Lys	
420 425 430	
gtt tct agt ttg agt gta gta agg tct tct gta agg caa aga aga aac	1343
Val Ser Ser Leu Ser Val Val Arg Ser Ser Val Arg Gln Arg Arg Asn	
435 440 445	
cca aag gaa act gct gat ctt tct agt gtc cag gaa ctt att gct gga	1391
Pro Lys Glu Thr Ala Asp Leu Ser Ser Val Gln Glu Leu Ile Ala Gly	
450 455 460	
gtt gac agc tgc tgc cat cca ggt atg ctg gag act gta agg aat tgc	1439
Val Asp Ser Cys Cys His Pro Gly Met Leu Glu Thr Val Arg Asn Cys	
465 470 475	
aca tat gtt gga atg gca gat gat gtt ttt gct tta gtt cag tat aac	1487
Thr Tyr Val Gly Met Ala Asp Asp Val Phe Ala Leu Val Gln Tyr Asn	
480 485 490 495	

acc cat cta tat cta gca aat gtg gtg aat ctc agc aaa gag cta atg	1535
Thr His Leu Tyr Leu Ala Asn Val Val Asn Leu Ser Lys Glu Leu Met	
500 505 510	
tat cag caa act ctt cgt cgt ttt gct cat ttt aac gca ata cag ctt	1583
Tyr Gln Gln Thr Leu Arg Arg Phe Ala His Phe Asn Ala Ile Gln Leu	
515 520 525	
agc gat cca gcc cct ttg tca gag ttg ata ttg ttg gct ctg aaa gag	1631
Ser Asp Pro Ala Pro Leu Ser Glu Leu Ile Leu Leu Ala Leu Lys Glu	
530 535 540	
gag gat cta gat cca gga aat gat aca aaa gat gat ctg aaa gaa aga	1679
Glu Asp Leu Asp Pro Gly Asn Asp Thr Lys Asp Asp Leu Lys Glu Arg	
545 550 555	
att gct gaa atg aat aca gaa ctc ctc aag gaa aaa gca gaa atg tta	1727
Ile Ala Glu Met Asn Thr Glu Leu Leu Lys Glu Lys Ala Glu Met Leu	
560 565 570 575	
gag gag tat ttc agc gtg cac att gac tcc agt gca aat ttg tca agg	1775
Glu Glu Tyr Phe Ser Val His Ile Asp Ser Ser Ala Asn Leu Ser Arg	
580 585 590	
ctt cct gtg ata ctc gac cag tat aca cct gac atg gat cgt gtt cct	1823
Leu Pro Val Ile Leu Asp Gln Tyr Thr Pro Asp Met Asp Arg Val Pro	
595 600 605	
gaa ttt tta cta tgc ttg gga aat gat gtt gag tgg gaa gat gag aag	1871
Glu Phe Leu Leu Cys Leu Gly Asn Asp Val Glu Trp Glu Asp Glu Lys	
610 615 620	
agt tgc ttt caa gga gtt tct gca gct att ggg aac ttt tac gcc atg	1919
Ser Cys Phe Gln Gly Val Ser Ala Ala Ile Gly Asn Phe Tyr Ala Met	
625 630 635	
cat cct cct ctt ttg cca aac cca tcg ggt gac ggt att cag ttc tat	1967
His Pro Pro Leu Leu Pro Asn Pro Ser Gly Asp Gly Ile Gln Phe Tyr	
640 645 650 655	
agt aag aga ggt gag agc tct cag gaa aag tca gat tta gag ggt aac	2015
Ser Lys Arg Gly Glu Ser Ser Gln Glu Lys Ser Asp Leu Glu Gly Asn	
660 665 670	
gtc gat atg gag gac aat ctt gac caa gat ctt ctg tca gat gct gaa	2063
Val Asp Met Glu Asp Asn Leu Asp Gln Asp Leu Leu Ser Asp Ala Glu	
675 680 685	
aac gca tgg gca caa cgt gaa tgg tca atc caa cac gtg ttg ttt ccg	2111
Asn Ala Trp Ala Gln Arg Glu Trp Ser Ile Gln His Val Leu Phe Pro	
690 695 700	
tca atg aga ttg ttc ttg aag cca cca gct tcc atg gct tca aat ggg	2159
Ser Met Arg Leu Phe Leu Lys Pro Pro Ala Ser Met Ala Ser Asn Gly	
705 710 715	

act ttt gta aag gta gca tcc ctt gaa aag ctg tac aag ata ttc gaa 2207
 Thr Phe Val Lys Val Ala Ser Leu Glu Lys Leu Tyr Lys Ile Phe Glu
 720 725 730 735

cga tgc taactgaaac cgctgattgt agaagaactt ttgatatgag tagcttccat 2263
 Arg Cys

ttgctctaac tatgtttcta gactttgaat gaaagtggaa ccagtttacg gttaaaccaa 2323
 actgtggcac acacgactga ccaaaacat aacaatcaaaa ctccaccttt tcctgtga 2381

<210> 4
 <211> 737
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4
 Met Ile Asp Asp Ser Ser Leu Thr Ala Glu Met Glu Glu Glu Glu Ser
 1 5 10 15
 Pro Ala Thr Thr Ile Val Pro Arg Glu Pro Pro Lys Ile Gln Arg Leu
 20 25 30
 Glu Glu Ser Val Val Asn Arg Ile Ala Ala Gly Glu Val Ile Gln Arg
 35 40 45
 Pro Val Ser Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala Asp
 50 55 60
 Ser Ser Ser Ile Ser Val Val Val Lys Asp Gly Gly Leu Lys Leu Ile
 65 70 75 80
 Gln Val Ser Asp Asp Gly His Gly Ile Arg Arg Glu Asp Leu Pro Ile
 85 90 95
 Leu Cys Glu Arg His Thr Thr Ser Lys Leu Thr Lys Phe Glu Asp Leu
 100 105 110
 Phe Ser Leu Ser Ser Met Gly Phe Arg Gly Glu Ala Leu Ala Ser Met
 115 120 125
 Thr Tyr Val Ala His Val Thr Val Thr Thr Ile Thr Lys Gly Gln Ile
 130 135 140
 His Gly Tyr Arg Val Ser Tyr Arg Asp Gly Val Met Glu His Glu Pro
 145 150 155 160
 Lys Ala Cys Ala Ala Val Lys Gly Thr Gln Ile Met Val Glu Asn Leu
 165 170 175
 Phe Tyr Asn Met Ile Ala Arg Arg Lys Thr Leu Gln Asn Ser Ala Asp
 180 185 190
 Asp Tyr Gly Lys Ile Val Asp Leu Leu Ser Arg Met Ala Ile His Tyr
 195 200 205
 Asn Asn Val Ser Phe Ser Cys Arg Lys His Gly Ala Val Lys Ala Asp
 210 215 220
 Val His Ser Val Val Ser Pro Ser Arg Leu Asp Ser Ile Arg Ser Val
 225 230 235 240
 Tyr Gly Val Ser Val Ala Lys Asn Leu Met Lys Val Glu Val Ser Ser
 245 250 255
 Cys Asp Ser Ser Gly Cys Thr Phe Asp Met Glu Gly Phe Ile Ser Asn
 260 265 270
 Ser Asn Tyr Val Ala Lys Lys Thr Ile Leu Val Leu Phe Ile Asn Asp
 275 280 285
 Arg Leu Val Glu Cys Ser Ala Leu Lys Arg Ala Ile Glu Ile Val Tyr
 290 295 300
 Ala Ala Thr Leu Pro Lys Ala Ser Lys Pro Phe Val Tyr Met Ser Ile
 305 310 315 320

